

SEQUENCE LISTING

<110> West, James W.
 Brandt, Cameron S.
 Jaspers, Stephen R.

 <120> Production of Homotrimeric Fusion
 Proteins

 <130> 02-17

 <150> 60/417,801
 <151> 2002-10-11

 <160> 22

 <170> FastSEQ for Windows Version 3.0

 <210> 1
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 <223> C-myc tag.

 <400> 1
 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
 1 5 10

 <210> 2
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 <223> Hemagglutinin A epitope tag

 <400> 2
 Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
 1 5

 <210> 3
 <211> 1377
 <212> DNA
 <213> Human

 <220>
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 <222> (14)...(892)

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 Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg
 1 5 10 49

 agc cgt gtg gac cag gag gag cgc ttt cca cag ggc ctg tgg acg ggg
 Ser Arg Val Asp Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly
 15 20 25 97

 gtg gct atg aga tcc tgc ccc gaa gag cag tac tgg gat cct ctg ctg 145

Val	Ala	Met	Arg	Ser	Cys	Pro	Glu	Glu	Gln	Tyr	Trp	Asp	Pro	Leu	Leu	
30						35					40					
ggt	acc	tgc	atg	tcc	tgc	aaa	acc	att	tgc	aac	cat	cag	agc	cag	cgc	193
Gly	Thr	Cys	Met	Ser	Cys	Lys	Thr	Ile	Cys	Asn	His	Gln	Ser	Gln	Arg	
45						50					55				60	
acc	tgt	gca	gcc	ttc	tgc	agg	tca	ctc	agc	tgc	cgc	aag	gag	caa	ggc	241
Thr	Cys	Ala	Ala	Phe	Cys	Arg	Ser	Leu	Ser	Cys	Arg	Lys	Glu	Gln	Gly	
65						70					75					
aag	ttc	tat	gac	cat	ctc	ctg	agg	gac	tgc	atc	agc	tgt	gcc	tcc	atc	289
Lys	Phe	Tyr	Asp	His	Leu	Leu	Arg	Asp	Cys	Ile	Ser	Cys	Ala	Ser	Ile	
80						85					90					
tgt	gga	cag	cac	cct	aag	caa	tgt	gca	tac	ttc	tgt	gag	aac	aag	ctc	337
Cys	Gly	Gln	His	Pro	Lys	Gln	Cys	Ala	Tyr	Phe	Cys	Glu	Asn	Lys	Leu	
95						100					105					
agg	agc	cca	gtg	aac	ctt	cca	cca	gag	ctc	agg	aga	cag	cgg	agt	gga	385
Arg	Ser	Pro	Val	Asn	Leu	Pro	Pro	Glu	Leu	Arg	Arg	Gln	Arg	Ser	Gly	
110						115					120					
gaa	gtt	gaa	aac	aat	tca	gac	aac	tcg	gga	agg	tac	caa	gga	ttg	gag	433
Glu	Val	Glu	Asn	Asn	Ser	Asp	Asn	Ser	Gly	Arg	Tyr	Gln	Gly	Leu	Glu	
125						130					135			140		
cac	aga	ggc	tca	gaa	gca	agt	cca	gct	ctc	ccg	ggg	ctg	aag	ctg	agt	481
His	Arg	Gly	Ser	Glu	Ala	Ser	Pro	Ala	Leu	Pro	Gly	Leu	Lys	Leu	Ser	
145						150					155					
gca	gat	cag	gtg	gcc	ctg	gtc	tac	agc	acg	ctg	ggg	ctc	tgc	ctg	tgt	529
Ala	Asp	Gln	Val	Ala	Leu	Val	Tyr	Ser	Thr	Leu	Gly	Leu	Cys	Leu	Cys	
160						165					170					
gcc	gtc	ctc	tgc	tgc	ttc	ctg	gtg	gcg	gtg	gcc	tgc	ttc	ctc	aag	aag	577
Ala	Val	Leu	Cys	Cys	Phe	Leu	Val	Ala	Val	Ala	Cys	Phe	Leu	Lys	Lys	
175						180					185					
agg	ggg	gat	ccc	tgc	tcc	tgc	cag	ccc	cgc	tca	agg	ccc	cgt	caa	agt	625
Arg	Gly	Asp	Pro	Cys	Ser	Cys	Gln	Pro	Arg	Ser	Arg	Pro	Arg	Gln	Ser	
190						195					200					
ccg	gcc	aag	tct	tcc	cag	gat	cac	gcg	atg	gaa	gcc	ggc	agc	cct	gtg	673
Pro	Ala	Lys	Ser	Ser	Gln	Asp	His	Ala	Met	Glu	Ala	Gly	Ser	Pro	Val	
205						210					215			220		
agc	aca	tcc	ccc	gag	cca	gtg	gag	acc	tgc	agc	ttc	tgc	ttc	cct	gag	721
Ser	Thr	Ser	Pro	Glu	Pro	Val	Glu	Thr	Cys	Ser	Phe	Cys	Phe	Pro	Glu	
225						230					235					
tgc	agg	gcg	ccc	acg	cag	gag	agc	gca	gtc	acg	cct	ggg	acc	ccc	gac	769
Cys	Arg	Ala	Pro	Thr	Gln	Glu	Ser	Ala	Val	Thr	Pro	Gly	Thr	Pro	Asp	
240						245					250					
ccc	act	tgt	gct	gga	agg	tgg	ggg	tgc	cac	acc	agg	acc	aca	gtc	ctg	817
Pro	Thr	Cys	Ala	Gly	Arg	Trp	Gly	Cys	His	Thr	Arg	Thr	Thr	Val	Leu	
255						260					265					
cag	cct	tgc	cca	cac	atc	cca	gac	agt	ggc	ctt	ggc	att	gtg	tgt	gtg	865
Gln	Pro	Cys	Pro	His	Ile	Pro	Asp	Ser	Gly	Leu	Gly	Ile	Val	Cys	Val	
270						275					280					

cct gcc cag gag ggg ggc cca ggt gca taaatggggg tcagggagggg	912
Pro Ala Gln Glu Gly Gly Pro Gly Ala	
285	290
aaaggaggag ggagagagat ggagaggagg ggagagagaa agagaggtgg ggagagggga	972
gagagatatg aggagagaga gacagaggag gcagaaaagg agagaaaacag aggagacaga	1032
gagggagaga gagacagagg gagagagaga cagaggggaa gagaggcaga gagggaaaaga	1092
ggcagagaag gaaaagaca ggcagagaag gagagaggca gagagggaga gagggcagaga	1152
gggagagagg cagagagaca gagagggaga gagggacaga gagagataga qcaggaggtc	1212
ggggcactct gagtcccagt tcccatgcg gctgttaggtc gtcatcacct aaccacacgt	1272
gcaataaaagt cctcgccct gctgctaca gcccccgaga gccccctcctc ctggagaata	1332
aacactttgg cagctgccct tcctcaaaaa aaaaaaaaaa aaaaa	1377
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<211> 293	
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<213> Human	
<400> 4	
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Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg	
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Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met	
35 40 45	
Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala	
50 55 60	
Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp	
65 70 75 80	
His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His	
85 90 95	
Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val	
100 105 110	
Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn	
115 120 125	
Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser	
130 135 140	
Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val	
145 150 155 160	
Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys	
165 170 175	
Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro	
180 185 190	
Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser	
195 200 205	
Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro	
210 215 220	
Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro	
225 230 235 240	
Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala	
245 250 255	
Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro	
260 265 270	
His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala Gln Glu	
275 280 285	
Gly Gly Pro Gly Ala	
290	
<210> 5	
<211> 21	

<212> DNA			
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<223> PCR primer			
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<212> DNA			
<213> Artificial Sequence			
<220>			
<223> PCR primer			
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acaggtgtcc agggaaattca tataggccgg ccaccatgga tgcaatgaag agaggg	56		
<210> 8			
<211> 36			
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accctcaggg atcgaacccg aacccgaacc ggatcc	36		
<210> 9			
<211> 118			
<212> DNA			
<213> Artificial Sequence			
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gatcggtatcc atggccgaaa ctgatcctaa aacagttcaa gaccttacca gcgttagtcca	60		
gacgctcctg caagagatcg aagataagtt tcagactatg agcgaccaaa tcatttag	118		
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<212> DNA			
<213> Artificial Sequence			
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acgcggatgtgttggaaaga gttggaaagga agtgggttcta	100	
<210> 11		
<211> 110		
<212> DNA		
<213> Artificial Sequence		
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gatcttagaac cacttccttc caactcttcc acaccagctt gcgtcattaa atctgctata	60	
tttttctcaa ggtcatctat cctggagctc atgtcatcgaa ttctctcaat	110	
<210> 12		
<211> 108		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> PCR primer		
<400> 12		
gattttggctcg ctcatgtct gaaacttatac ttgcattctct tgcaggagcg tctggactac	60	
gctggtaagg tcttgaactg ttttaggatc agtttcggcc atggatcc	108	
<210> 13		
<211> 33		
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<213> Artificial Sequence		
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<223> PCR primer		
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cacacgtacg aagatggatg caatgaagag agg	33	
<210> 14		
<211> 30		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> PCR primer		
<400> 14		
ggtagatct cgaacccgaa cccgaaccgg	30	
<210> 15		
<211> 62		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> PCR primer		
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ctagaatataa ttttgtttaa cttaagaag gagatataata tatggctatg agatcctgcc	60	
cc	62	

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<210> 16
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 16
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ggcc                                     64

<210> 17
<211> 516
<212> DNA
<213> Artificial Sequence

<220>
<223> TACI-HSBP fragment

<400> 17
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tcctgcaaaa ccattgcaa ccatcagagc cagcgcaccc gtgcagccctt ctgcaggta      120
ctcagctgcc gcaaggagca aggcaagtcc tatgaccatc tcctgaggga ctgcattcagc      180
tgtgcctcca tctgtggaca gcaccctaag caatgtgcat acttctgtga gaacaagctc      240
aggagcggat ccgggtcggg ttccgggtcg agatccatgg ccgaaactga tcctaaaaca      300
gttcaagacc ttaccagcgt agtccagacg ctcctgcaag agatgcaaga taagttcag      360
actatgagcg accaaatcat tgagagaatc gatgacatga gctccaggat agatgaccctt      420
gagaaaaata tagcagattt aatgacgcaa gctgggtgtgg aagagttgga aggaagtgg      480
tctagatccg gtggccatca ccatcaccat cactga                                516

<210> 18
<211> 171
<212> PRT
<213> Artificial Sequence

<220>
<223> TACI-HSBP fragment

<400> 18
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Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
20          25          30
Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
35          40          45
Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
50          55          60
Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
65          70          75          80
Arg Ser Gly Ser Gly Ser Gly Ser Arg Ser Met Ala Glu Thr
85          90          95
Asp Pro Lys Thr Val Gln Asp Leu Thr Ser Val Val Gln Thr Leu Leu
100         105         110
Gln Glu Met Gln Asp Lys Phe Gln Thr Met Ser Asp Gln Ile Ile Glu
115         120         125
Arg Ile Asp Asp Met Ser Ser Arg Ile Asp Asp Leu Glu Lys Asn Ile
130         135         140
Ala Asp Leu Met Thr Gln Ala Gly Val Glu Glu Leu Glu Gly Ser Gly
145         150         155         160
Ser Arg Ser Gly Gly His His His His His
165         170

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<210> 19
<211> 480
<212> DNA
<213> Artificial Sequence

<220>
<223> NC-1 fragment

<221> CDS
<222> (1)...(480)

<400> 19
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Met Pro Glu Gly Phe Ile Lys Ala Gly Gln Arg Pro Ser Leu Ser Gly
 1           5           10          15

acc cct ctt gtt agt gcc aac cag cgg gta aca gga atg cct gtg tct      96
Thr Pro Leu Val Ser Ala Asn Gln Arg Val Thr Gly Met Pro Val Ser
 20          25          30

gct ttt act gtt att ctc tcc aaa gct tac cca gca ata gga act ccc      144
Ala Phe Thr Val Ile Leu Ser Lys Ala Tyr Pro Ala Ile Gly Thr Pro
 35          40          45

ata cca ttt gat aaa att ttg tat aac agg caa cag cat tat gac cca      192
Ile Pro Phe Asp Lys Ile Leu Tyr Asn Arg Gln Gln His Tyr Asp Pro
 50          55          60

agg act gga atc ttt act tgt cag ata cca gga ata tac tat ttt tca      240
Arg Thr Gly Ile Phe Thr Cys Gln Ile Pro Gly Ile Tyr Tyr Phe Ser
 65          70          75          80

tac cac gtg cat gtg aaa ggg act cat gtt tgg gta ggc ctg tat aag      288
Tyr His Val His Val Lys Gly Thr His Val Trp Val Gly Leu Tyr Lys
 85          90          95

aat ggc acc cct gta atg tac acc tat gat gaa tac acc aaa ggc tac      336
Asn Gly Thr Pro Val Met Tyr Thr Tyr Asp Glu Tyr Thr Lys Gly Tyr
100          105          110

ctg gat cag gct tca ggg agt gcc atc atc gat ctc aca gaa aat gac      384
Leu Asp Gln Ala Ser Gly Ser Ala Ile Ile Asp Leu Thr Glu Asn Asp
115          120          125

cag gtg tgg ctc cag ctt ccc aat gcc gag tca aat ggc cta tac tcc      432
Gln Val Trp Leu Gln Leu Pro Asn Ala Glu Ser Asn Gly Leu Tyr Ser
130          135          140

tct gag tat gtc cac tcc tct ttc tca gga ttc cta gtg gct cca atg      480
Ser Glu Tyr Val His Ser Ser Phe Ser Gly Phe Leu Val Ala Pro Met
145          150          155          160

<210> 20
<211> 160
<212> PRT
<213> Artificial Sequence

<220>
<223> NC-1 fragment

<400> 20

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 Ala Phe Thr Val Ile Leu Ser Lys Ala Tyr Pro Ala Ile Gly Thr Pro
 35 40 45
 Ile Pro Phe Asp Lys Ile Leu Tyr Asn Arg Gln Gln His Tyr Asp Pro
 50 55 60
 Arg Thr Gly Ile Phe Thr Cys Gln Ile Pro Gly Ile Tyr Tyr Phe Ser
 65 70 75 80
 Tyr His Val His Val Lys Gly Thr His Val Trp Val Gly Leu Tyr Lys
 85 90 95
 Asn Gly Thr Pro Val Met Tyr Thr Tyr Asp Glu Tyr Thr Lys Gly Tyr
 100 105 110
 Leu Asp Gln Ala Ser Gly Ser Ala Ile Ile Asp Leu Thr Glu Asn Asp
 115 120 125
 Gln Val Trp Leu Gln Leu Pro Asn Ala Glu Ser Asn Gly Leu Tyr Ser
 130 135 140
 Ser Glu Tyr Val His Ser Ser Phe Ser Gly Phe Leu Val Ala Pro Met
 145 150 155 160

<210> 21
<211> 195
<212> DNA
<213> Artificial Sequence

<220>
<223> HSBP-1 fragment

<221> CDS
<222> (1)...(195)

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Met Ala Glu Thr Asp Pro Lys Thr Val Gln Asp Leu Thr Ser Val Val	
1 5 10 15	

cag acg ctc ctg caa gag atg caa gat aag ttt cag act atg agc gac	96
Gln Thr Leu Leu Gln Glu Met Gln Asp Lys Phe Gln Thr Met Ser Asp	
20 25 30	

caa atc att gag aga atc gat gac atg agc tcc agg ata gat gac ctt	144
Gln Ile Ile Glu Arg Ile Asp Asp Met Ser Ser Arg Ile Asp Asp Leu	
35 40 45	

gag aaa aat ata gca gat tta atg acg caa gct ggt gtg gaa gag ttg	192
Glu Lys Asn Ile Ala Asp Leu Met Thr Gln Ala Gly Val Glu Glu Leu	
50 55 60	

gaa	195
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<210> 22
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<212> PRT
<213> Artificial Sequence

<220>
<223> HSBP-1 fragment

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20 25 30
Gln Ile Ile Glu Arg Ile Asp Asp Met Ser Ser Arg Ile Asp Asp Leu
35 40 45
Glu Lys Asn Ile Ala Asp Leu Met Thr Gln Ala Gly Val Glu Glu Leu
50 55 60
Glu
65